

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Adams, Craig W.  
Pang, Patty P.-Y.  
Belei, Marina

(ii) TITLE OF INVENTION: Recombinant DNase B Derived from  
Streptococcus pyogenes

(iii) NUMBER OF SEQUENCES: 16

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sheldon & Mak  
(B) STREET: 225 South Lake Avenue, Ninth Floor  
(C) CITY: Pasadena  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91001

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/\_\_\_\_, \_\_\_\_
- (B) FILING DATE:
- (C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Farber, Michael B.
- (B) REGISTRATION NUMBER: 32,612
- (C) REFERENCE/DOCKET NUMBER: 9521

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (818) 796-4000
- (B) TELEFAX: (818) 795-6321

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: NO

## (v) FRAGMENT TYPE: N-terminal

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys Arg Leu

1                      5                      10                      15

Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala Val Thr

20                      25                      30

Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg

35                      40

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic DNA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAACGGATCC GAATCTACTT GGATCAAGAC GGGTTTTTTC T

41

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic DNA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGGTCGAC CCGGGGAATG ACGGCAATCA TTGCTTTTTC T

41

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Xaa

1

5

10

15

Tyr Leu Asn Glu Ala Leu Ala

20

(2) INFORMATION. FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAUACNCART NWSNAAYGAY GT

22

(2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser  
1 5 10 15

Lys Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn  
20 25 30

Tyr Tyr Lys Thr Leu Gly  
35

(2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 129..944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACAACGCCT TCTTTTTTCT CCTTACTATC TCCTTTAATT TTCATATTTT TTAAAAAAC 60

TATTGATAAA CTAGTTAAGT AAGCGTATAC TATGGTTAGT TAGCGAAATT AGAAAAGAGG 120



ACAAGCAT ATG AAT CTA CTT GGA TCA AGA CGG GTT TTT TCT AAA AAA TGT 170

Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys

1

5

10

CGG CTA GTA AAA TTT TCA ATG GTA GCT CTT GTA TCA GCC ACA ATG GCT 218

Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala

15

20

25

30

GTA ACA ACA GTC ACA CTT GAA AAT ACT GCA CTG GCA CGA CAA ACA CAG 266

Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg Gln Thr Gln

35

40

45

GTC TCA AAT GAT GTT GTT CTA AAT GAT GGC GCA AGC AAG TAC CTA AAC 314

Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn

50

55

60

GAA GCA TTA GCT TGG ACA TTC AAT GAC AGT CCT AAC TAT TAC AAA ACT 362

Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr

65

70

75

TTA GGT ACT AGT CAG ATT ACT CCA GCA CTC TTT CCT AAA GCA GGA GAT 410

Leu Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp

80

85

90

ATT CTC TAT AGC AAA TTA GAT GAG TTA GGA AGG ACG CGT ACT GCT AGA 458

Ile Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg

95

100

105

110

GGT ACA TTG ACT TAT GCC AAT GTT GAA GGT AGC TAC GGT GTT AGA CAA 506  
 Gly Thr Leu Thr Tyr Ala Asn Val Glu Gly Ser Tyr Gly Val Arg Gln  
 115 120 125

TCT TTC GGT AAA AAT CAA AAC CCC GCA GGA TGG ACT GGA AAC CCT AAT 554  
 Ser Phe Gly Lys Asn Gln Asn Pro Ala Gly Trp Thr Gly Asn Pro Asn  
 130 135 140

CAT GTC AAA TAT AAA ATT GAA TGG TTA AAT GGT CTA TCT TAT GTC GGA 602  
 His Val Lys Tyr Lys Ile Glu Trp Leu Asn Gly Leu Ser Tyr Val Gly  
 145 150 155

GAT TTC TGG AAT AGA AGT CAT CTC ATT GCA GAT AGT CTC GGT GGA GAT 650  
 Asp Phe Trp Asn Arg Ser His Leu Ile Ala Asp Ser Leu Gly Gly Asp  
 160 165 170

GCA CTC AGA GTC AAT GCC GTT ACA GGA ACA CGT ACC CAA AAT GTA GGA 698  
 Ala Leu Arg Val Asn Ala Val Thr Gly Thr Arg Thr Gln Asn Val Gly  
 175 180 185 190

GGT CGT GAC CAA AAA GGC GGC ATG CGC TAT ACC GAA CAA AGA GCT CAA 746  
 Gly Arg Asp Gln Lys Gly Gly Met Arg Tyr Thr Glu Gln Arg Ala Gln  
 195 200 205

GAA TGG TTA GAA GCA AAT CGT GAT GGC TAT CTT TAT TAT GAA GTC GCT 794  
 Glu Trp Leu Glu Ala Asn Arg Asp Gly Tyr Leu Tyr Tyr Glu Val Ala  
 210 215 220

CCA ATC TAC AAC GCA GAC GAG TTG ATT CCA AGA GCT GTC GTG GTA TCA 842  
 Pro Ile Tyr Asn Ala Asp Glu Leu Ile Pro Arg Ala Val Val Val Ser  
 225 230 235

ATG CAA TCT TCT GAT AAT ACC ATC AAC GAG AAA GTA TTA GTT TAC AAC 890  
 Met Gln Ser Ser Asp Asn Thr Ile Asn Glu Lys Val Leu Val Tyr Asn  
 240 245 250

ACA GCT AAT GGC TAC ACC ATT AAC TAC CAT AAC GGT ACA CCT ACT CAA 938  
 Thr Ala Asn Gly Tyr Thr Ile Asn Tyr His Asn Gly Thr Pro Thr Gln  
 255 260 265 270

AAA TAATACCAAA AGGCTAGACC TCTGCTCACT AGGCCTAGCT TTTTACATCA 991  
 Lys

AAAAAAGCAA TGACTATAGA AAGTAAAAAT ACTAGAAAAA GCAATGATTG CCGTCATTGC 1051

TTTTTATGAA TTTGTGCAAA AAGCAAAAAA GC 1083

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Leu Leu, Gly Ser Arg Arg Val Phe Ser Lys Lys Cys Arg Leu

1 5 10 15

Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala Val Thr

20 25 30

Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg Gln Thr Gln Val Ser

35 40 45

Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn Glu Ala

50 55 60

Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr Leu Gly

65 70 75 80

Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp Ile Leu

85 90 95

Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg Gly Thr

100 105 110

Leu Thr Tyr Ala Asn Val Glu Gly Ser Tyr Gly Val Arg Gln Ser Phe

115 120 125

Gly Lys Asn Gln Asn Pro Ala Gly Trp Thr Gly Asn Pro Asn His Val

130

135

140

Lys Tyr Lys Ile Glu Trp Leu Asn Gly Leu Ser Tyr Val Gly Asp Phe

145

150

155

160

Trp Asn Arg Ser His Leu Ile Ala Asp Ser Leu Gly Gly Asp Ala Leu

165

170

175

Arg Val Asn Ala Val Thr Gly Thr Arg Thr Gln Asn Val Gly Gly Arg

180

185

190

Asp Gln Lys Gly Gly Met Arg Tyr Thr Glu Gln Arg Ala Gln Glu Trp

195

200

205

Leu Glu Ala Asn Arg Asp Gly Tyr Leu Tyr Tyr Glu Val Ala Pro Ile

210

215

220

Tyr Asn Ala Asp Glu Leu Ile Pro Arg Ala Val Val Val Ser Met Gln

225

230

235

240

Ser Ser Asp Asn Thr Ile Asn Glu Lys Val Leu Val Tyr Asn Thr Ala

245

250

255

Asn Gly Tyr Thr Ile Asn Tyr His Asn Gly Thr Pro Thr Gln Lys

260

265

270

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser  
1                      5                      10                      15

Lys Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn  
                    20                      25                      30

Tyr Tyr Lys Thr Leu Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro  
                    35                      40                      45

Lys Ala Gly Asp Ile Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr

50

55

60

Arg Thr Ala Arg Gly Thr Leu Thr Tyr Ala Asn Val Glu Gly Ser Tyr

65

70

75

80

Gly Val Arg Gln Ser Phe Gly Lys Asn Gln Asn Pro Ala Gly Trp Thr

85

90

95

Gly Asn Pro Asn His Val Lys Tyr Lys Ile Glu Trp Leu Asn Gly Leu

100

105

110

Ser Tyr Val Gly Asp Phe Trp Asn Arg Ser His Leu Ile Ala Asp Ser

115

120

125

Leu Gly Gly Asp Ala Leu Arg Val Asn Ala Val Thr Gly Thr Arg Thr

130

135

140

Gln Asn Val Gly Gly Arg Asp Gln Lys Gly Gly Met Arg Tyr Thr Glu

145

150

155

160

Gln Arg Ala Gln Glu Trp Leu Glu Ala Asn Arg Asp Gly Tyr Leu Tyr

165

170

175

Tyr Glu Val Ala Pro Ile Tyr Asn Ala Asp Glu Leu Ile Pro Arg Ala

180

185

190

Val Val Val Ser Met Gln Ser Ser Asp Asn Thr Ile Asn Glu Lys Val

195

200

205

Leu Val Tyr Asn Thr Ala Asn Gly Tyr Thr Ile Asn Tyr His Asn Gly

210

215

220

Thr Pro Thr Gln Lys

225

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GACAACGCCT TCTTTTTTCT CTTACTATC TCCTTTAATT TTCATATTTT TTAAAAAAC 60  
TATTGATAAA CTAGTTAAGT AAGCGTATAC TATGGTTAGT TAGCGAAATT AGAAAAGAGG 120  
ACAAGCATAT GAATCTACTT GGATCAAGAC GGGTTTTTTC TAAAAAATGT CGGCTAGTAA 180  
AATTTTCAAT GGTAGCTCTT 200

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGATCCGA ATCTACTTGG ATCAAGACGG GTTTTTTCTA AAAAATGTCG GCTAGTAAAA 60

TTTTCAATGG TAGCTCTTGT ATCAGCCACA ATGGCTGTAA CAACAGTCAC ACTTGAAAAT 120

ACTGCACTGG CACGACAAAC ACAGGTCTCA AATGATGTTG TTCTAAATGA TGGCGCAAGC 180

AAGTACCTAA ACGAAGCATT AGCTTGGACA TTCAATGACA GTCCTAACTA TTACAAAAC 240

TTAGGTACTA GTCAGATTAC TCCAGCACTC TTTCCTAAAG CAGGAGATAT TCTCTATAGC 300

AAATTAGATG AGTTAGGAAG GACGCGTACT GCTAGAGGTA CATTGACTTA TGCCAATGTT 360

GAAGGTAGCT ACGGTGTTAG ACAATCTTTC GGTA AAAATC AAAACCCCGC AGGATGGACT 420

GGAAACCCTA ATCATGTCAA ATATAAAATT GAATGGTTAA ATGGTCTATC TTATGTCGGA 480

GATTTCTGGA ATAGAAGTCA TCTCATTGCA GATAGTCTCG GTGGAGATGC ACTCAGAGTC 540

AATGCCGTTA CAGGAACACG TACCCAAAAT GTAGGAGGTC GTGACCAAAA AGGCGGCATG 600

CGCTATACCG AACAAAGAGC TCAAGAATGG TTAGAAGCAA ATCGTGATGG CTATCTTTAT 660

TATGAAGTCG CTCCAATCTA CAACGCAGAC GAGTTGATTC CAAGAGCTGT CGTGGTATCA 720

ATGCAATCTT CTGATAATAC CATCAACGAG AAAGTATTAG TTTACAACAC AGCTAATGGC 780

TACACCATTA ACTACCATAA CGGTACACCT ACTCAAAAAT AATACCAGAA GGCTAGACCT 840

CTGCTCACTA GGCCTAGCTT TTTACATCAA AAAAAGCAAT GACTATAGAA AGTAAAAATA 900

CTAGAAAAAG CAATGATTGC CGTCATTGCC CCGGGTCGAC 940

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGCAATGGA TCCGAACCTG CTGGGTTCCT GTCGTGTTTT CTCCAAAAAA TGCCGTCTGG 60

TTAAATTCTC CATGGTTGCT CTGGTTTCCG CTACCATGGC TGTTACCACC GTTACCCTGG 120

AAAACACCGC TCTGGCTCAG ACACAGGTCT CAAATGATGT TGTTCTAAAT GATGGCGCAA 180

GC 182

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGGTCGAC CCGGGGCAAT GACGGCAATC ATTGCTTTTC T 41

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	GAT	CCG	AAC	CTG	CTG	GGT	TCC	CGT	CGT	GTT	TTC	TCC	AAA	AAA	TGC	48
Met	Asp	Pro	Asn	Leu	Leu	Gly	Ser	Arg	Arg	Val	Phe	Ser	Lys	Lys	Cys	
1				5					10						15	

CGT CTG GTT AAA TTC TCC ATG GTT GCT CTG GTT TCC GCT ACC ATG GCT 96

Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala

20

25

30

GTT ACC ACC GTT ACC CTG GAA AAC ACC GCT CTG GCT CAG ACA CAG GTC 144

Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Gln Thr Gln Val

35

40

45

TCA AAT GAT GTT GTT CTA AAT GAT GGC GCA AGC AAG TAC CTA AAC GAA 192

Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn Glu

50

55

60

GCA TTA GCT TGG ACA TTC AAT GAC AGT CCT AAC TAT TAC AAA ACT TTA 240

Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr Leu

65

70

75

80

GGT ACT AGT CAG ATT ACT CCA GCA CTC TTT CCT AAA GCA GGA GAT ATT 288

Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp Ile

85

90

95

CTC TAT AGC AAA TTA GAT GAG TTA GGA AGG ACG CGT ACT GCT AGA GGT 336

Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg Gly

100

105

110

ACA TTG ACT TAT GCC AAT GTT GAA GGT AGC TAC GGT GTT AGA CAA TCT 384

Thr Leu Thr Tyr Ala Asn Val Glu Gly Ser Tyr Gly Val Arg Gln Ser

115

120

125

TTC GGT AAA AAT CAA AAC CCC GCA GGA TGG ACT GGA AAC CCT AAT CAT 432  
 Phe Gly Lys Asn Gln Asn Pro Ala Gly Trp Thr Gly Asn Pro Asn His  
 130 135 140

GTC AAA TAT AAA ATT GAA TGG TTA AAT GGT CTA TCT TAT GTC GGA GAT 480  
 Val Lys Tyr Lys Ile Glu Trp Leu Asn Gly Leu Ser Tyr Val Gly Asp  
 145 150 155 160

TTC TGG AAT AGA AGT CAT CTC ATT GCA GAT AGT CTC GGT GGA GAT GCA 528  
 Phe Trp Asn Arg Ser His Leu Ile Ala Asp Ser Leu Gly Gly Asp Ala  
 165 170 175

CTC AGA GTC AAT GCC GTT ACA GGA ACA CGT ACC CAA AAT GTA GGA GGT 576  
 Leu Arg Val Asn Ala Val Thr Gly Thr Arg Thr Gln Asn Val Gly Gly  
 180 185 190

CGT GAC CAA AAA GGC GGC ATG CGC TAT ACC GAA CAA AGA GCT CAA GAA 624  
 Arg Asp Gln Lys Gly Gly Met Arg Tyr Thr Glu Gln Arg Ala Gln Glu  
 195 200 205

TGG TTA GAA GCA AAT CGT GAT GGC TAT CTT TAT TAT GAA GTC GCT CCA 672  
 Trp Leu Glu Ala Asn Arg Asp Gly Tyr Leu Tyr Tyr Glu Val Ala Pro  
 210 215 220

ATC TAC AAC GCA GAC GAG TTG ATT CCA AGA GCT GTC GTG GTA TCA ATG 720  
 Ile Tyr Asn Ala Asp Glu Leu Ile Pro Arg Ala Val Val Val Ser Met  
 225 230 235 240

CAA TCT TCT GAT AAT ACC ATC AAC GAG AAA GTA TTA GTT TAC AAC ACA 768  
 Gln Ser Ser Asp Asn Thr Ile Asn Glu Lys Val Leu Val Tyr Asn Thr  
 245 250 255

GCT AAT GGC TAC ACC ATT AAC TAC CAT AAC GGT ACA CCT ACT CAA AAA 816  
 Ala Asn Gly Tyr Thr Ile Asn Tyr His Asn Gly Thr Pro Thr Gln Lys  
 260 265 270

TAATACCAAA AGGCTAGACC TCTGCTCACT AGGCCTAGCT TTTTACATCA AAAAAAGCAA 876

TGACTATAGA AAGTAAAAAT ACTAGAAAAA GCAATGATTG CCGTCATTGC CCCGGGTCGA 936

C 937

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:



Met Asp Pro Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys  
 1 5 10 15

Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala  
 20 25 30

Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Gln Thr Gln Val  
 35 40 45

Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn Glu  
 50 55 60

Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr Leu  
 65 70 75 80

Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp Ile  
 85 90 95

Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg Gly  
 100 105 110

Thr Leu Thr Tyr Ala Asn Val Glu Gly Ser Tyr Gly Val Arg Gln Ser  
 115 120 125

Phe Gly Lys Asn Gln Asn Pro Ala Gly Trp Thr Gly Asn Pro Asn His  
 130 135 140

Val Lys Tyr Lys Ile Glu Trp Leu Asn Gly Leu Ser Tyr Val Gly Asp

145 150 155 160

Phe Trp Asn Arg Ser His Leu Ile Ala Asp Ser Leu Gly Gly Asp Ala

165 170 175

Leu Arg Val Asn Ala Val Thr Gly Thr Arg Thr Gln Asn Val Gly Gly

180 185 190

Arg Asp Gln Lys Gly Gly Met Arg Tyr Thr Glu Gln Arg Ala Gln Glu

195 200 205

Trp Leu Glu Ala Asn Arg Asp Gly Tyr Leu Tyr Tyr Glu Val Ala Pro

210 215 220

Ile Tyr Asn Ala Asp Glu Leu Ile Pro Arg Ala Val Val Val Ser Met

225 230 235 240

Gln Ser Ser Asp Asn Thr Ile Asn Glu Lys Val Leu Val Tyr Asn Thr

245 250 255

Ala Asn Gly Tyr Thr Ile Asn Tyr His Asn Gly Thr Pro Thr Gln Lys

260 265 270

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys

1

5

10

15

Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr

20

25

30